

Amendments to the Specification:

Please replace paragraph [0047] with the following amended paragraph:

[0047]Herein, the phrase "complementary to a nucleotide sequence" encompasses not only cases wherein a nucleotide sequence completely pairs with the template, but also includes those that have at least 70%, preferably 80%, more preferably 90%, and even more preferably 95% or more (for example, 97% or 99%) of the nucleotides paired with the template. Pairing refers to the formation of a chain in which T (U in the case of RNAs) corresponds to A, A corresponds to T or U, G corresponds to C, and C corresponds to G in the nucleotide sequence of the template polynucleotide. Homologies at the nucleotide sequence level between certain polynucleotides can be determined by the BLAST algorithm (Altschul (1990) Proc. Natl. Acad. Sci. USA 87: 2264-8; Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90: 5873-7). The BLASTN program for nucleotide sequences (Altschul et al. (1990) J. Mol. Biol. 215: 403-410) has been developed based on this algorithm, and can be used to determine the homology of marker polynucleotide probe sequences (see <http://www.worldwideweb.ncbi.nlm.nih.gov> for a specific example of analysis methods).

Please replace paragraph [0051] with the following amended paragraph:

[0051]References such as Molecular Cloning, A Laboratory Manual 2.sup.nd ed. (Cold Spring Harbor Press (1989); Section 9.47-9.58), Current Protocols in Molecular Biology (John Wiley & Sons (1987-1997); Section 6.3-6.4), DNA Cloning 1: Core Techniques, A Practical Approach 2.sup.nd ed. (Oxford University (1995); Section 2.10 for conditions, in particular), can be referred to for detailed information on hybridization procedures. Examples of hybridizing polynucleotides include polynucleotides containing a nucleotide sequence that has at least 50% or more, preferably 70%, more preferably 80% and even more preferably 90% (for example, 95% or more, or 99%) identity with a nucleotide sequence comprising the nucleotides of SEQ ID NO: 1 or SEQ ID NO: 2. Such identities can be determined by the BLAST algorithm (Altschul (1990) Proc. Natl. Acad. Sci. USA 87: 2264-8; Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90: 5873-7) as described in the homology determination above. In addition to the above-described BLASTN program for nucleotide sequences, the BLASTX program for determining

the identity of amino acid sequences (Altschul et al. (1990) J. Mol. Biol. 215: 403-10) and the like has been developed based on this algorithm and can be used (as described above, see <http://www.worldwideweb.ncbi.nlm.nih.gov>. for a specific example of analysis methods).

Please replace paragraph [0121] with the following amended paragraph:

[0121]Gene expression regulatory regions can be predicted using a program such as Neural Network (http://www.fruitfly.org/seg_tools/promoter.html; Reese et al., Biocomputing: Proceedings of the 1996 Pacific Symposium, Hunter and Klein ed., World Scientific Publishing Co., Singapore, (1996)). Moreover, a program for predicting the minimum unit required for the activity of an expression regulatory region is also known and can be used (<http://worldwideweb.biosci.cbs.umn.edu/software/proscan/promotescan.htm>; Prestridge (1995) J. Mol. Biol. 249: 923-932).

Please replace paragraph [0131] with the following amended paragraph:

[0131]The nucleotide sequence of an siRNA can be designed using a computer program such as that disclosed at the Ambion website (http://www.worldwideweb.ambion.coni/techlib/misc/siRNA_finder.html). Kits for screening for functional siRNAs are also commercially available and can be used (for example, BD Knockout RNAi System (BD Biosciences Clontech).